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MHC Variation Sculpts Individualized Microbial Communities That Control Susceptibility to Enteric Infection

Supplementary Information

Authors: Jason L. Kubinak^{1,†}, W. Zac Stephens¹, Ray Soto¹, Charisse Petersen¹, Tyson Chiaro¹, Lasha Gogokhia¹, Rickesha Bell¹, Nadim J. Ajami^{3,4}, Joseph F. Petrosino^{3,4}, Linda Morrison², Wayne K. Potts², Peter E. Jensen¹, Ryan M. O'Connell¹, and June L. Round^{1,†}

Author Affiliations: ¹Department of Pathology, Division of Microbiology and Immunology, University of Utah School of Medicine, Salt Lake City, UT 84112

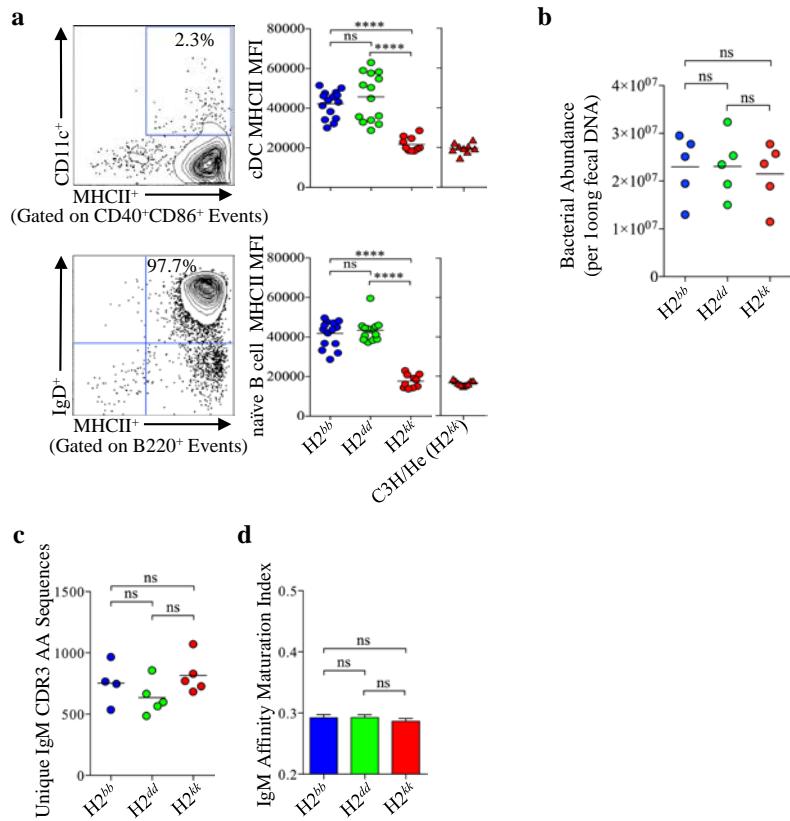
²Department of Biology, University of Utah, Salt Lake City, UT 84112

³Department of Molecular Virology and Microbiology, Baylor College of Medicine, Houston, TX 77030

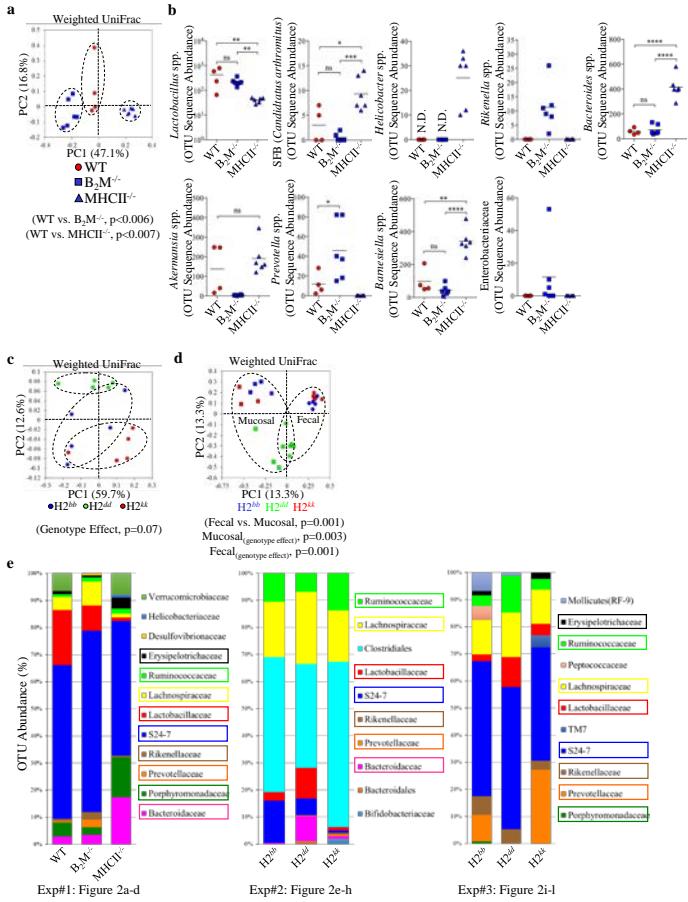
⁴Alkek Center for Metagenomics and Microbiome Research, Baylor College of Medicine, Houston, TX 77030

[†]Corresponding Authors: (jason.kubinak@path.utah.edu; june.round@path.utah.edu)

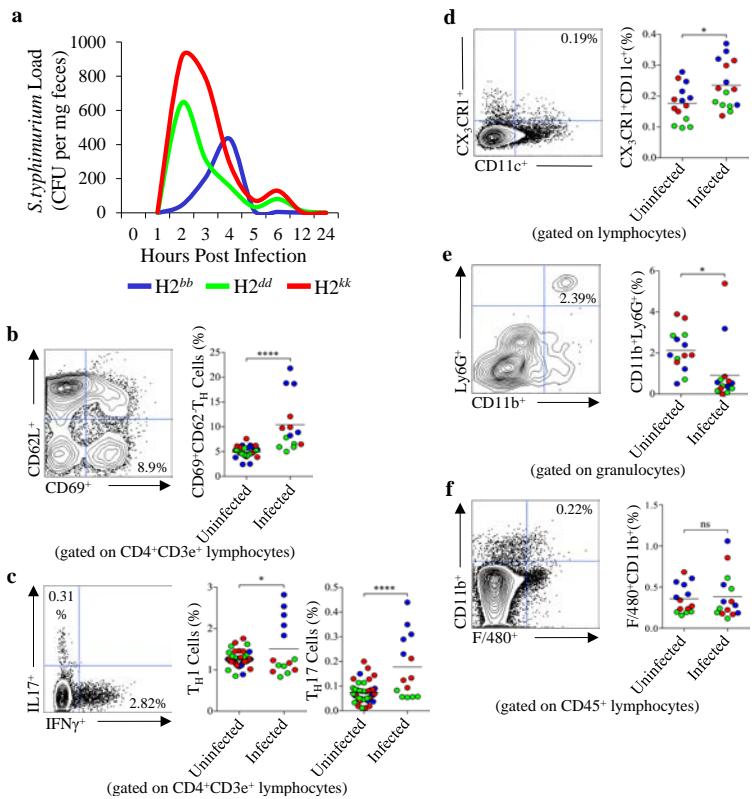
Supplementary Figures



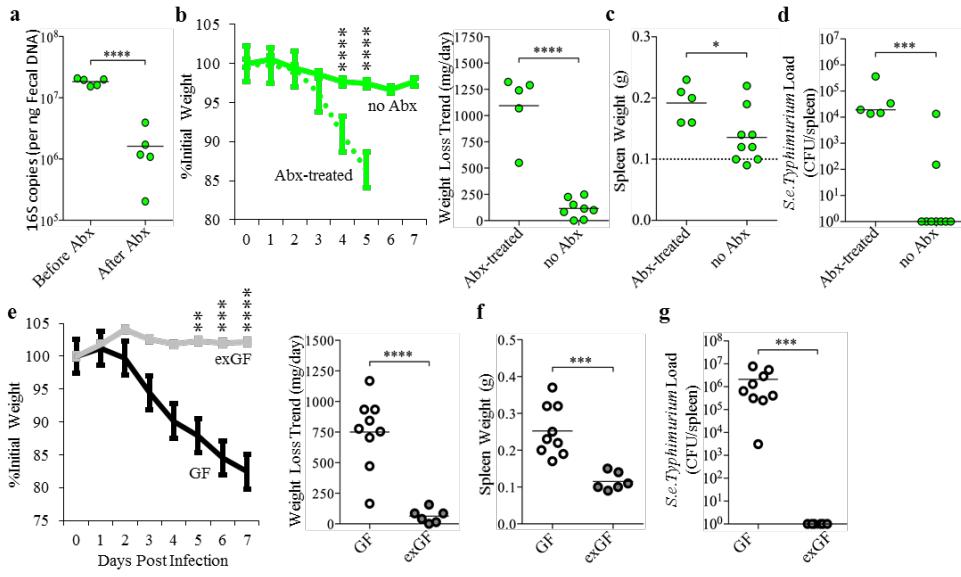
Supplementary Figure 1 | MHC mediates IgA response against gut microbiota. (a) Representative F.C. plots and data sets comparing the relative surface expression of MHC on dendritic cells and naïve B cells from MHC congenic animals ($H2^{bb}$ -n=15; $H2^{dd}$ -n=14; $H2^{kk}$ -n=15, C3H/HeJ-n=9). (b) There is no difference in the relative abundance of fecal bacteria in H2 congenic animals ($H2^{bb}$ -n=5, $H2^{dd}$ -n=5, $H2^{kk}$ -n=5). (c,d) Comparison of naïve IgM repertoire among MHC genotypes ($H2^{bb}$ -n=4, $H2^{dd}$ -n=5, $H2^{kk}$ -n=5). There is no difference between MHC genotypes when (c) sequence diversity and (d) affinity maturation scores of the naïve IgM repertoire are compared among MHC genotypes. (a-c) Bars represent group means. (d) Error bars represent S.E.M. A two-tailed unpaired Student's t-test was used for all pair-wise statistical comparisons (**p<0.00001; ***p<0.001; **p<0.01; *p<0.05).



Supplementary Figure 2 | MHC sculpts microbiota composition in the gut. (a) PcoA plot based on weighted UniFrac analysis of fecal microbiotas from WT, B₂M^{-/-}, and MHCII^{-/-} animals. (b) OTU abundance plots of specific bacterial groups among WT, B₂M^{-/-}, and MHCII^{-/-} animals. “N.D.”=not detected. All pairwise comparisons are results of Student’s t-test (****=p<0.0001; ***=p<0.001; **=p<0.01; *p<0.05). (c) PcoA plot based on weighted UniFrac analysis of fecal microbiotas from female H2 congenic animals. (d) PcoA plot based on weighted UniFrac analysis of fecal microbiotas from male H2 congenic animals used for comparison of fecal and microbiota communities. (a,c,d) P-values represent the results of a PERMANOVA based on 999 simulations. Ellipses in PcoA plots are for illustrative purposes only and are non-quantitative. (e) Stacked bar charts represent relative abundance among significantly differentially detected OTUs within each bacterial clade. Bacterial families consistently enriched for significant MHC effects across the independent experiments described in Figure 2 are highlighted by colored boxes (see Supplementary Tables 4-6 Data 1 for full list of OTUs and results of kruskal-wallis statistical tests).

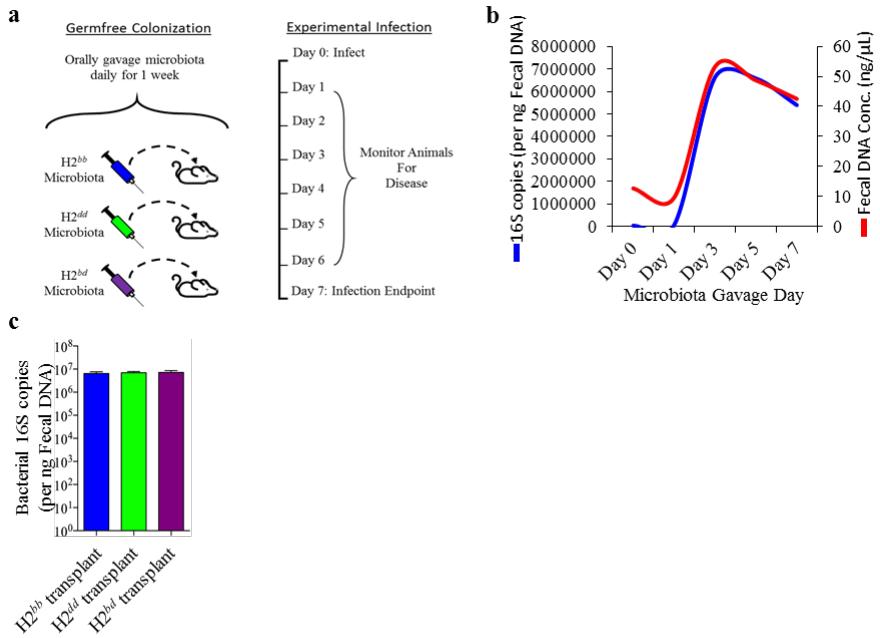


Supplementary Figure 3 | MHC mediates susceptibility to *S.e.typhimurium* infection and this is not due to an enhanced immune response in resistant genotypes. (a) Qualitative analysis of Salmonella loads in the feces of mice ($n=3-5$ per genotype) at defined time-points after oral gavage of 10^4 CFUs. Fecal pellets were collected at each time point, homogenized with pestle, and plated on MacConkey agar. Salmonella loads are standardized per mg feces. A smoothed trendline is shown. (b,c) Results of F.C. experiments demonstrating that infection of H2^{bb} ($n=5$), but not H2^{dd} ($n=5$) or H2^{kk} ($n=5$), elicits an immune response as measured by increases in the abundance of (b) activated CD4⁺ T_H cells, and (c) inflammatory T_H1 and T_H17 cells. (d-f) Results of F.C. experiments demonstrating that infection does not result from differential recruitment of phagocytes (CX₃CR1⁺CD11c⁺ monocytes, Ly6G⁺CD11b⁺ neutrophils, CD11b⁺F/480⁺ macrophages) among H2 congenic genotypes. (b-f) Representative F.C. plots are provided for all F.C. data sets (percentages are provided to identify relevant subgate). Unpaired two-tailed Student's t-test (****= $p<0.0001$; ***= $p<0.001$; **= $p<0.01$; *= $p<0.05$).

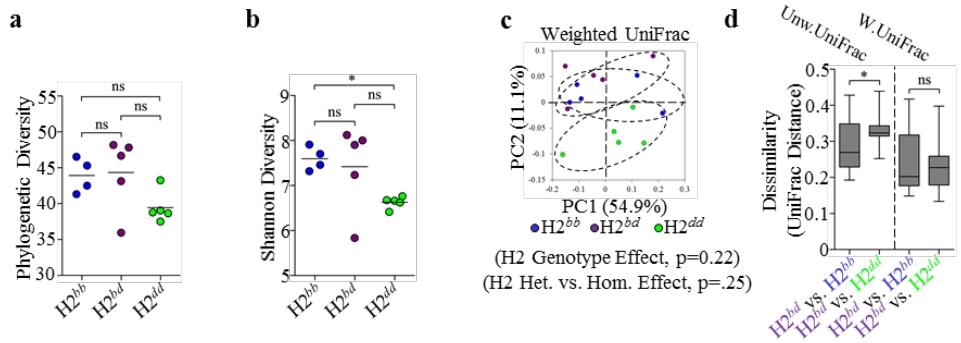


Supplementary Figure 4 | Susceptibility to *S.e.typhimurium* infection is microbiota-

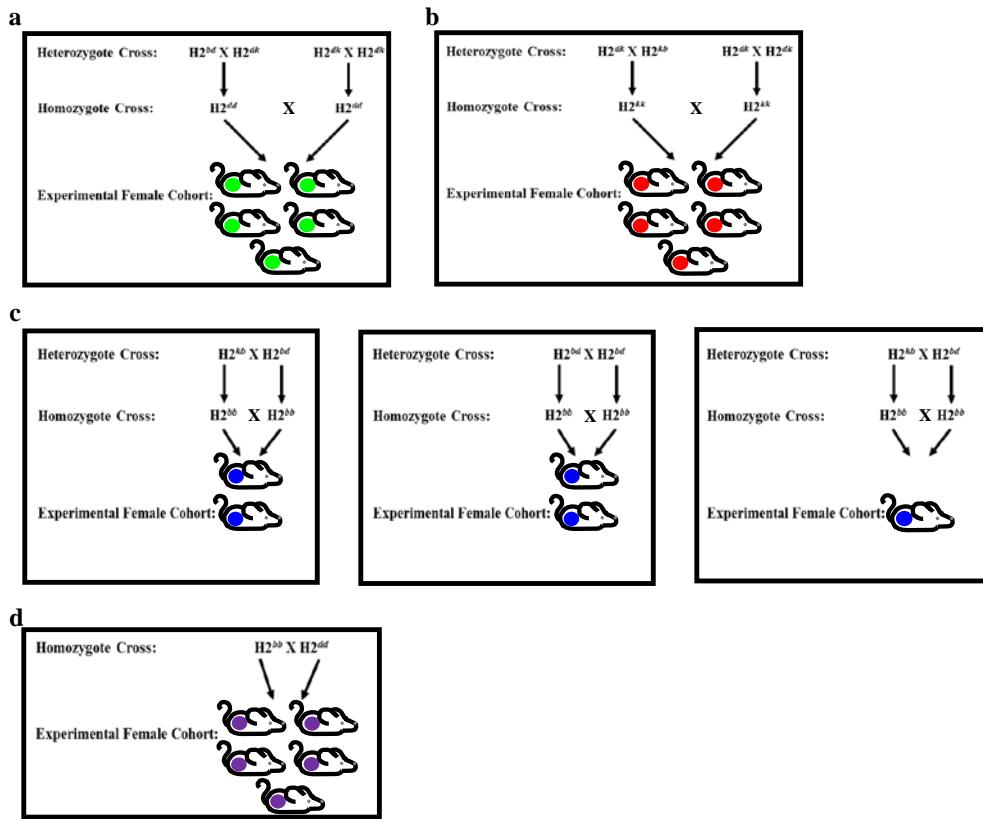
dependent. (a-d) Disease scores from Salmonella-infected (10^4 CFU via oral gavage) resistant $H2^{dd}$ animals, and $H2^{dd}$ animals that had been administered antibiotics in their drinking water for 3 days (0.5mg/mL of each of the following: Neomycin Sulfate, Ampicillin, Erythromycin, Gentamycin). Animals were taken off antibiotics 24 hours prior to infecting with 10^4 *S.e.typhimurium* CFUs via oral gavage. (e-g) Disease scores of Salmonella-infected (10^4 CFU via oral gavage) GF animals and animals that were born GF and were subsequently reared from birth in and SPF facility until 9 weeks of age (i.e. exGF). (b-right panel, c, e-right panel, f) Results of unpaired two-tailed Student's t-test ($****=p<0.0001$; $**=p<0.01$; $*=p<0.05$). (b and e (left panels)) Error bars represent S.E.M. Asterisks represent significant differences based on results of t-tests comparing weight loss by day and reflect significant differences between Abx-treated and untreated $H2^{dd}$ animals in (b) and GF and exGF animals in (e). (d and g) Asterisks represent significance based on results of Mann-Whitney U Test, ($***=p<0.001$).



Supplementary Figure 5 | Fecal transplants recapitulate patterns of susceptibility in colonized GF animals. (a) Illustration for design of microbiota colonization, and Salmonella infection experiments. (b) Dynamics of microbiota colonization of GF animals as inferred from fecal bacterial loads and increasing fecal DNA concentrations over the course of 7 day colonizations (T_0 -n=4; T_1 -n=2; T_3 -n=2; T_5 -n=1; T_7 -n=19). (c) Results of Q-PCR experiment quantifying fecal bacterial loads in GF animals that had been colonized with microbiota derived from $H2^{bb}$ (n=8), $H2^{dd}$ (n=4), and $H2^{bd}$ (n=7)(Day 7 time-point).



Supplementary Figure 6 | MHC heterozygosity influences microbiota composition. (a) PCoA plot based on weighted UniFrac analysis of fecal microbiotas from H2^{bb}, H2^{bd}, and H2^{dd} animals. The reported p-values represent the results of a PERMANOVA based on 999 simulations testing the effect of host genotype, or homozygosity versus heterozygosity. (b,c) Within-community estimates of (b) phylogenetic diversity and (c) Shannon diversity. (d) Distance boxplots of community similarity between H2^{bd} heterozygotes and each respective H2^{bb} and H2^{dd} homozygote parent strains based on unweighted and weighted UniFrac analysis. (b-d) Unpaired two-tailed Student's t-test ($p<0.05=*$).



Supplementary Figure 7 | Breeding design for female MHC congenic mice used for microbiota sequencing experiment described in Figure 2e-h. The experiments described in Figure 2e-h and 4a represents the results of a single experiment where 5 animals from each of the three different MHC genotypes had their microbiotas sequenced. **(a)** In the case of the $H2^{dd}$ (green dotted mice) and **(b)** $H2^{kk}$ (red dotted mice) animals, the 5 animals from each genotype were both litter- and cage-mates (i.e. for each genotype, 5 female animals from the same litter were housed in the same cage and used for analysis). **(c)** The $H2^{bb}$ animals (blue dotted mice) represent five female animals derived from three different mothers that were housed in three separate cages. This design provides an internal control for the possibility that drift or maternal effects significantly influences our results by demonstrating that $H2^{bb}$ animals still significantly cluster by genotype when compared to the other two $H2$ congenic cohorts. **(a-c)** Re-deriving homozygote congenic breeder pairs from heterozygote crosses, and using their progeny for microbiota sequencing analysis, excludes the confounding effect of the independent husbandry of these strains for several decades (the strain isolation effect). **(d)** 5 heterozygous $H2^{bb}$ animals (purple dotted mice) depicted in Figure 4a were derived from a single breeder pair ($H2^{dd} \times H2^{bb}$ cross) which exposes animals to both $H2^{bb}$ and $H2^{dd}$ microbiota.

Supplementary Tables

Supplementary Table 1. MHC Haplotypes of H2 congenic BALB/c mice

Locus	Class Ia		Class IIa			Class Ia	
	K	A β	A α	E β	E α	D	L
H2 ^d haplotype	d	d	d	d	d	d	d
H2 ^b haplotype	b	b	b	b	^	b	b
H2 ^k haplotype	k	k	k	k	k	k	^

^: null allele

Adapted from ¹

Supplementary Table 2. Cell Subset, Markers, and Antibodies used for flow cytometry

Cell Subset	Markers
CD4 ⁺ T _H Cells	CD4 ⁺ CD3ε ⁺
CD8 ⁺ T _{CT} Cells	CD8α ⁺ CD3ε ⁺
Activated CD4 ⁺ T _H Cells	CD4 ⁺ CD3ε ⁺ CD62L ⁺ CD69 ⁺
Activated CD8 ⁺ T _{CT} Cells	CD8α ⁺ CD3ε ⁺ CD62L ⁺ CD69 ⁺
Tolerogenic Dendritic Cells	CD11c ⁺ CD103 ⁺
T _{reg} Cells	CD4 ⁺ CD3ε ⁺ FoxP3 ⁺
IL10 ⁺ Treg Cells	CD4 ⁺ CD3ε ⁺ FoxP3 ⁺ IL10 ⁺
T _{H1} Cells	CD4 ⁺ CD3ε ⁺ IFNγ ⁺
T _{H17} Cells	CD4 ⁺ CD3ε ⁺ IL17 ⁺
T _{FH} Cells	CD4 ⁺ CD3ε ⁺ CXCR5 ⁺ PD1 ⁺
Naïve B Cells	B220 ⁺ IgD ^{hi} MHCII ⁺
GC B Cells	B220 ⁺ IgD ^{lo} GL7 ⁺ FAS ⁺
IgA ⁺ B Cells	B220 ⁺ CD138 IgA ⁺
IgA ⁺ Plasma Cells	B220 ⁺ CD138 ⁺ IgA ⁺
Conventional Dendritic Cells	CD40 ⁺ CD86 ⁺ CD11c ⁺ MHCII ⁺

CD4-FITC ([1/250 dilution, clone](#) RM4-5,eBioscience [cat#11-0042](#)) CD8α-PerCP.Cy5.5 ([1/250 dilution, clone](#) 53-6.7,BioLegend [cat#100733](#)); CD3ε-Pacific Blue ([1/250 dilution, clone](#) 145-2C11,eBioscience [cat#48-0031](#)); CD62L-PE ([1/250 dilution, clone](#) MEL-14,BioLegend [cat#104407](#)); CD69-PE/Cy7 ([1/250 dilution, clone](#) H1.2F3,BioLegend [cat#104511](#)); CD11c-APC ([1/250 dilution, clone](#) N418,eBioscience [cat#17-0114](#)); CD103-PE ([1/250 dilution, clone](#) 2E7,BioLegend [cat#121405](#)); FoxP3-APC ([1/50 dilution, clone](#) FJK-16s,eBioscience [cat#45-5773](#)); IL10-PE ([1/50 dilution, clone](#) JES5-16E3,eBioscience [cat#12-7101](#)); IFNγ-PE ([1/50 dilution, clone](#) XMG1.2,BioLegend [cat#505807](#)); IL17A-eFluor660 ([1/250 dilution, clone](#) eBio17B7,eBioscience [cat#50-7177](#)); CXCR5-PE ([1/250 dilution, clone](#) SPRCL5,eBioscience [cat#12-7185](#)); CXCR5 isotype control Rat IgG2a-PE ([1/250 dilution, clone](#) eBR2a,eBioscience [cat#9012-4321](#)); PD1-PE/Cy7 ([1/250 dilution, clone](#) RMP1-30,BioLegend [cat#109109](#)); PD1 isotype control Rat IgG2b-PE/Cy7 ([1/250 dilution, clone](#) RTK4530,BioLegend [cat#400617](#)); B220-PerCP.Cy5.5 ([1/500 dilution, clone](#) RA3-6B2,BioLegend [cat#103235](#)); IgD-AlexaFluor647 ([1/250 dilution, clone](#) 11-26c.2a,BioLegend [cat#405707](#)); MHCII(IA/IE)-PE ([1/250 dilution, clone](#) M5/114.15.2,BioLegend [cat#107607](#)); MHCII-IA^k-PE ([1/250 dilution, clone](#) 10-3.6,BioLegend [cat#109908](#)); MHCII isotype control Rat IgG2b-PE ([1/250 dilution, clone](#) eB149,eBioscience [cat#12-4031](#)); GL7-AlexaFluor488 ([1/250 dilution, clone](#) GL-7,eBioscience [cat#53-5902](#)); FAS-PE/Cy7 ([1/250 dilution, clone](#) Jo2,BD Biosciences [cat#557653](#)); CD138-PE ([1/250 dilution, clone](#) 281-2,BioLegend [cat#142503](#)); Rat anti-mouse IgA-PE ([1/500 dilution, SouthernBiotech \[catalog#1165-09L\]\(#\)](#)); CD40-FITC ([1/250 dilution, clone](#) HM40-3,BioLegend [cat#102905](#)); CD86-PerCP.Cy5.5 ([1/250 dilution, clone](#) GL-1,BioLegend [cat#105027](#)); Goat anti-mouse IgA-FITC ([1/250 dilution, SouthernBiotech \[cat#1040-02\]\(#\)](#))

Notes on antibody staining:

-IgA-PE was used to quantify IgA-bound fecal bacteria
-FoxP3-PerCP.Cy5.5 was used to stain Tregs in PPs

-The IA/IE antibody does not bind IA molecules from mice carrying the H₂^{kk} haplotype. To overcome this, an IA^k-specific antibody was mixed with the IA/IE antibody in all MHCII stains.

Supplementary Table 3. Primers used in study

Use	Target	Sequence (1,2)	Reference
Bacterial qPCR	Eubacteria	Forward: 5-ACTCCTACGGGAGGCAGCAGT-3	2
		Reverse: 5-ATTACCGCGGCTGCTGGC-3	
Bacterial qPCR	Bacteroides/Prevotella spp.	Forward: 5-CCTWCGATGGATAGGGTT-3	3
		Reverse: 5-CACGCTACTTGGCTGGTCAG-3	
Bacterial qPCR	Lactobacillus/Lactococcus spp.	Forward: 5-AGCAGTAGGGAATCTCCA-3	4
		Reverse: 5-CACCGCTACACATGGAG-3	
Ig repertoire cDNA synthesis, first PCR	IgA C _H Region	AACTGGCTGCTCATGGTGTACC	
Ig repertoire cDNA synthesis, first PCR	IgD C _H Region	TATGGTGCAAGTGTGGTTGAGG	
Ig repertoire cDNA synthesis, first PCR	IgG C _H Region	CTGGACAGGGMTCCAAGATTC	
Ig repertoire cDNA synthesis, first PCR	IgM C _H Region	CTCTGGGAGACAGCAASACC	
Ig repertoire, first PCR	Ig V _H Regions	ACACTCTTCCCTACACGACGCTCTCCGATCT(N ₁₉₋₂₁)	5
Ig repertoire, second PCR	Ig first PCR product	AATGATAACGGCACCACCGAGATCTACACXXXXXXXXX ACACTCTTCCCTACACGACGC	
Ig repertoire, second PCR	Ig first PCR product – IgA C _H	CAAGCAGAACGGCATACGAGATXXXXXXXXGTGAC TGGAGTTCAACGTGTGCTCTCCGATCTGATGGTGGG ATTTCTCGCAGA	
Ig repertoire, second PCR	Ig first PCR product – IgD C _H	CAAGCAGAACGGCATACGAGATXXXXXXXXGTG ACTGGAGTTCAACGTGTGCTCTCCGATCTGGGCT TTGCACTGTAGAGG	
Ig repertoire, second PCR	Ig first PCR product – IgG C _H	CAAGCAGAACGGCATACGAGATXXXXXXXX XGTGACTGGAGTTCAACGTGTGCTCTCCGA TCTGGRCCARKGGATAGACHGATG	
Ig repertoire, second PCR	Ig first PCR product – IgM C _H	CAAGCAGAACGGCATACGAGATXXXXXXXX TGACTGGAGTTCAACGTGTGCTCTCCGATCTG GGAAGACATTGGGAAGGAC	

1. N₁₉₋₂₁ represents the 17 “external” primers identified by Rohatgi et al., 2008 to target the 16 different V_H region families.

2. **Bold** sequences are Illumina adapter sequences. XXXXXXXXX represents index sequences.

Supplementary Table References

- 1 Flurkey, K., Currer, J. M., Leiter, E. H. & Witham, B. (The Jackson Laboratory, Bar Harbor, ME, 2009).
- 2 Amann, R. I. *et al.* Combination of 16S rRNA-targeted oligonucleotide probes with flow cytometry for analyzing mixed microbial populations. *Applied and environmental microbiology* **56**, 1919-1925 (1990).
- 3 Furet, J. P. *et al.* Comparative assessment of human and farm animal faecal microbiota using real-time quantitative PCR. *FEMS microbiology ecology* **68**, 351-362, doi:10.1111/j.1574-6941.2009.00671.x (2009).
- 4 Rinttilä, T., Kassinen, A., Malinen, E., Krogus, L. & Palva, A. Development of an extensive set of 16S rDNA-targeted primers for quantification of pathogenic and indigenous bacteria in faecal samples by real-time PCR. *Journal of applied microbiology* **97**, 1166-1177, doi:10.1111/j.1365-2672.2004.02409.x (2004).
- 5 Rohatgi, S., Ganju, P. & Sehgal, D. Systematic design and testing of nested (RT-)PCR primers for specific amplification of mouse rearranged/expressed immunoglobulin variable region genes from small number of B cells. *Journal of immunological methods* **339**, 205-219, doi:10.1016/j.jim.2008.09.017 (2008).

Supplementary Table 4. WT, B2M-/-, MHCII-/- Significant differences by OTU*

OTU	Test-Statistic	P	FDR_P	WT mean	B2M_KO mean	MHCII_KO mean	taxonomy
FJ50363 3	14.11764 71	0.000859 79	0.050162 4	0	0	2.8333333 3	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__Bacteroidaceae;__Bacteroides
EU6558 86	13.27433 63	0.001310 73	0.052582 72	0.5	8.33333333	170	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__Bacteroidaceae;__Bacteroides
EF09704 2	13.12111 8	0.001415 09	0.052582 72	6.75	43.5	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__Bacteroidaceae;__Bacteroides
FJ95962 0	11.86036 04	0.002658	0.052582	0	0.33333333	3	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__Bacteroidaceae;__Bacteroides
GQ4482 46	11.85374 15	0.002666 81	0.052582 72	0	0.33333333	3	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__Bacteroidaceae;__Bacteroides
DQ8073 72	11.78557 54	0.002759 27	0.052582 72	8.5	0	13.833333 3	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__Bacteroidaceae;__Bacteroides
DQ8090 36	11.11111 11	0.003865 92	0.052582 72	0	0	1	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__Bacteroidaceae;__Bacteroides
EU4537 26	11.06406 48	0.003957 94	0.052582 72	34.75	17.3333333	204.83333 3	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__Bacteroidaceae;__Bacteroides
EU7678 93	10.89324 62	0.004310 84	0.052582 72	0	0	2	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__Bacteroidaceae;__Bacteroides
EU7662 74	10.88417 24	0.004330 44	0.052582 72	6.25	0	0.8333333 3	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__Bacteroidaceae;__Bacteroides
JN08419 8	9.122807 02	0.010447 39	0.085003 73	0	0.16666667	2	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__Bacteroidaceae;__Bacteroides
EU4571 66	11.78203 24	0.002764 17	0.052582 72	96.5	42.5	341.16666 7	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__Porphyromonadaceae;__Barnesiella
EU6557 28	11.28716 74	0.003540 16	0.052582 72	3.25	4.33333333	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__Porphyromonadaceae;__Odoribacter
EU5053 66	14.00778 21	0.000908 34	0.050162 4	0	7.16666667	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__Porphyromonadaceae;__Parabacteroides
HQ7915 02	11.11111 11	0.003865 92	0.052582 72	0	1	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__Porphyromonadaceae;__Parabacteroides
AY9931 53	13.98058 25	0.000920 78	0.050162 4	0	11.5	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__Prevotellaceae;__g
EU5050 99	13.98058 25	0.000920 78	0.050162 4	0	16	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__Prevotellaceae;__Prevotella
EF09748 2	12.27193 32	0.002163 63	0.052582 72	11.75	29.6666667	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__Prevotellaceae;__Prevotella
EU4519 86	14.00778 21	0.000908 34	0.050162 4	0	5.33333333	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__Rikenellaceae;__Alistipes
DQ8159 37	11.55213 27	0.003100 89	0.052582 72	0.25	0.5	4.8333333 3	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__Rikenellaceae;__Alistipes
EU4580 21	10.84940 65	0.004406 37	0.052582 72	14.75	0.83333333	10.5	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__Rikenellaceae;__Alistipes
EU6557 22	14.09001 96	0.000871 75	0.050162 4	0	36.1666667	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__Rikenellaceae;__RC9_gut_group

EF09721 1	14.00778 21	0.000908 34	0.050162 4	0	6.5	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__Rikenellaceae;__Rikenella
EU6558 56	10.91703 06	0.004259 88	0.052582 72	0	4.83333333	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__Rikenellaceae;__Rikenella
EU5047 17	14.65648 85	0.000656 73	0.050162 4	2.75	0	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EU6558 10	14.65648 85	0.000656 73	0.050162 4	8.25	0	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EF09761 8	14.61928 93	0.000669 05	0.050162 4	4.75	0	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EF09983 1	14.61928 93	0.000669 05	0.050162 4	6.75	0	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EU7604 49	14.61928 93	0.000669 05	0.050162 4	144.7 5	0	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EU5049 81	14.03508 77	0.000896 02	0.050162 4	0	0	7.3333333	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EU4537 33	14.00778 21	0.000908 34	0.050162 4	0	5.5	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EU5044 71	14.00778 21	0.000908 34	0.050162 4	0	3	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EU6560 52	13.98058 25	0.000920 78	0.050162 4	0	19.6666667	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EU5044 01	13.98058 25	0.000920 78	0.050162 4	0	0	7.3333333	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EU5054 58	13.98058 25	0.000920 78	0.050162 4	0	317.166667	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
JQ08511 5	13.53383 46	0.001151 24	0.052582 72	0	6.33333333	88.8333333	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EU5101 33	13.43283 58	0.001210 87	0.052582 72	0	10.3333333	26.8333333	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EU5100 97	13.12111 8	0.001415 09	0.052582 72	10.75	4.83333333	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EU5106 67	13.05803 57	0.001460 44	0.052582 72	0.25	16.6666667	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EU5120 10	12.70676 69	0.001740 85	0.052582 72	19.5	7.83333333	1	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EF09752 0	12.68768 77	0.001757 53	0.052582 72	3.25	0.66666667	15.1666666	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EF09649 8	12.67079 03	0.001772 45	0.052582 72	5.5	2.16666667	28	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EU5050 62	12.63346 83	0.001805 83	0.052582 72	113.7 5	14.1666667	166	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EF40677 8	12.53709 2	0.001894 98	0.052582 72	3.75	17.5	104.166666	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EF40653 4	12.46312 68	0.001966 38	0.052582 72	19.75	9.33333333	100	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EF09706 9	12.14165 26	0.002309 26	0.052582 72	12.75	1	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EF40678	12.09499	0.002363	0.052582	28.5	11.5	118	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g

9	26	77	72				
EU4546 18	12.09499 26	0.002363 77	0.052582 72	134.7 5	36	98.166666 7	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EF40675 4	12.03223 27	0.002439 12	0.052582 72	1.25	0.16666667	3.5	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EU4514 65	11.98998 18	0.002491 2	0.052582 72	0	0.16666667	1.8333333 3	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EF09733 5	11.98687 13	0.002495 08	0.052582 72	13.5	2.33333333	21.666666 7	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
FJ87949 0	11.91063 17	0.002592 02	0.052582 72	0	2.16666667	6.1666666 7	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EU4514 03	11.75571 77	0.002800 78	0.052582 72	1.75	3.5	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EF09748 3	11.66537 27	0.002930 19	0.052582 72	21.25	19.3333333	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EU5048 30	11.61440 68	0.003005 82	0.052582 72	3.5	1	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EF09698 9	11.47286 82	0.003226 25	0.052582 72	104.5	86.6666667	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EU4555 95	11.44907 41	0.003264 86	0.052582 72	10	4	41.166666 7	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EU4559 19	11.44907 41	0.003264 86	0.052582 72	8.5	4.66666667	46.666666 7	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EU5044 74	11.43565 32	0.003286 85	0.052582 72	24	0	12	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EU4552 84	11.31716 42	0.003487 46	0.052582 72	32.25	7.83333333	15	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EF09983 2	10.91703 06	0.004259 88	0.052582 72	0	2	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EU4541 28	10.89324 62	0.004310 84	0.052582 72	0	2.33333333	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EU5054 19	10.89324 62	0.004310 84	0.052582 72	0	0	3.1666666 7	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EU5045 08	10.88573 04	0.004327 07	0.052582 72	1	13.1666667	1.1666666 7	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
AM9326 33	10.86956 52	0.004362 18	0.052582 72	0	54.8333333	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EU7910 64	10.86956 52	0.004362 18	0.052582 72	0	10.3333333	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EF40640 1	10.86552 75	0.004371 41	0.052582 42	14	16.8333333	0.8333333 3	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EF09698 4	10.75367 65	0.004622 41	0.054640 88	37	147.5	55	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EF40685 4	10.69340 33	0.004763 84	0.055785 88	10.25	4.16666667	0.8333333 3	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EU4577 78	10.38461 54	0.005559 16	0.063323 92	16.75	5	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EF09684 6	10.32206 12	0.005735 79	0.064127 85	2.25	4.16666667	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g

EU5046 03	10.28571 43	0.005840 98	0.064127 85	1.75	0	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EU7909 90	10.25316 46	0.005936 82	0.064127 85	3.5	0	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EF09920 3	10.10846 22	0.006382 27	0.068350 32	0.75	0	1.6666666 7	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EF09751 0	10.01956 18	0.006672 37	0.070256 08	0	1.16666667	4	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EF60304 0	9.971153 85	0.006835 83	0.071377 49	2.75	1.33333333	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EF09746 5	9.889705 88	0.007119 96	0.073729 85	3.25	2.66666667	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EF09819 5	9.827330 51	0.007345 52	0.075442 06	3	1	0.6666666 7	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EF09723 8	9.742702 1	0.007663 01	0.077899 22	9.5	9.16666667	0.5	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EU5046 47	9.694852 94	0.007848 55	0.078049 47	169.5	325.833333	137.66666 7	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EF09783 7	9.649493 24	0.008028 59	0.078592 35	3.75	1.5	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EF09713 5	9.597423 51	0.008240 36	0.079424 35	0	0.83333333	2.1666666 7	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EU5050 87	9.495759 59	0.008670 06	0.081173 58	25.75	49.1666667	20.166666 7	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EF09711 2	9.298245 61	0.009569 99	0.085003 73	0.25	0	3	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EF09705 2	9.298245 61	0.009569 99	0.085003 73	0.25	3	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EF09757 7	9.239130 43	0.009857 08	0.085003 73	9.5	6.83333333	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EU5045 69	9.239130 43	0.009857 08	0.085003 73	33.5	19.6666667	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EU5050 67	9.200892 86	0.010047 35	0.085003 73	4	26.5	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
DQ0149 20	9.179090 21	0.010157 48	0.085003 73	1.5	5.16666667	2.3333333 3	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EF09993 7	9.152173 91	0.010295 1	0.085003 73	2.25	0.16666667	0.5	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
AM9325 66	9.137134 05	0.010372 81	0.085003 73	8.25	2	0.5	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EF40646 2	9.041889 48	0.010878 74	0.086546 91	0.75	0.16666667	1.8333333 3	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EU5041 42	9.035539 22	0.010913 34	0.086546 91	0.25	0	1.5	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EU5081 78	9.000224 42	0.011107 75	0.087534 66	0.75	0	2.6666666 7	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
EF09802 8	8.816831 68	0.012174 45	0.095341 16	0.25	1.33333333	0	Bacteria;__Bacteroidetes;__Bacteroidia;__Bacteroidales;__S24-7;__g
JQ08395	9.730707	0.007709	0.077899	5.75	7.33333333	0	Bacteria;__Cyanobacteria;__4C0d-2;__o;__f;__g

3	4	1	22				
DQ8238 70	8.792792 79	0.012321 66	0.095894 68	0.5	0	2	Bacteria;__Cyanobacteria;__4C0d-2;__o;__f;__g
EU4522 06	12.27436 82	0.002161	0.052582 72	0	2	0.1666666 7	Bacteria;__Firmicutes;__Bacilli;__Lactobacillales;__Lactobacillaceae;__Lactobacillus
EU4555 51	12.26171 02	0.002174 72	0.052582 72	12.25	0.16666667	0	Bacteria;__Firmicutes;__Bacilli;__Lactobacillales;__Lactobacillaceae;__Lactobacillus
EU5051 98	11.87888 2	0.002633 5	0.052582 72	83.5	32.6666667	0	Bacteria;__Firmicutes;__Bacilli;__Lactobacillales;__Lactobacillaceae;__Lactobacillus
EU5052 61	11.86046 51	0.002657 86	0.052582 72	249.7 5	92.1666667	0	Bacteria;__Firmicutes;__Bacilli;__Lactobacillales;__Lactobacillaceae;__Lactobacillus
DQ8158 10	11.69463 73	0.002887 63	0.052582 72	0.25	0.83333333	10.333333 3	Bacteria;__Firmicutes;__Bacilli;__Lactobacillales;__Lactobacillaceae;__Lactobacillus
EU4528 61	11.59159 16	0.003040 31	0.052582 72	0	10.6666667	3.1666666 7	Bacteria;__Firmicutes;__Bacilli;__Lactobacillales;__Lactobacillaceae;__Lactobacillus
EF09792 5	11.57317 55	0.003068 43	0.052582 72	37.75	15.5	0	Bacteria;__Firmicutes;__Bacilli;__Lactobacillales;__Lactobacillaceae;__Lactobacillus
HM3635 37	11.54508 2	0.003111 84	0.052582 72	0	0.5	4	Bacteria;__Firmicutes;__Bacilli;__Lactobacillales;__Lactobacillaceae;__Lactobacillus
EU4536 43	11.25	0.003606 56	0.052582 72	0.5	0.5	5.3333333 3	Bacteria;__Firmicutes;__Bacilli;__Lactobacillales;__Lactobacillaceae;__Lactobacillus
EU5087 95	11.11290 32	0.003862 46	0.052582 72	8.25	2.66666667	0	Bacteria;__Firmicutes;__Bacilli;__Lactobacillales;__Lactobacillaceae;__Lactobacillus
EU4513 76	11.11153 26	0.003865 11	0.052582 72	0	7.16666667	2	Bacteria;__Firmicutes;__Bacilli;__Lactobacillales;__Lactobacillaceae;__Lactobacillus
EU5073 17	9.417892 16	0.009014 27	0.082444 41	3.25	0.83333333	0	Bacteria;__Firmicutes;__Bacilli;__Lactobacillales;__Lactobacillaceae;__Lactobacillus
EU4528 56	9.236641 22	0.009869 36	0.085003 73	0	10.5	2.8333333 3	Bacteria;__Firmicutes;__Bacilli;__Lactobacillales;__Lactobacillaceae;__Lactobacillus
EU4531 56	9.194528 88	0.010079 37	0.085003 73	0	8.66666667	2.5	Bacteria;__Firmicutes;__Bacilli;__Lactobacillales;__Lactobacillaceae;__Lactobacillus
EU5049 25	10.31201 25	0.005764 68	0.064127 85	3	0.5	9.3333333 3	Bacteria;__Firmicutes;__Clostridia;__Clostridiales;__Clostridiaceae;__Candidatus_Arthromit us
EU4545 63	12.47892 07	0.001950 91	0.052582 72	0	0.33333333	3.8333333 3	Bacteria;__Firmicutes;__Clostridia;__Clostridiales;__Family_XIII_Incertae_Sedis;__Incertae Sedis
EF09850 7	14.09001 96	0.000871 75	0.050162 4	0	3.33333333	0	Bacteria;__Firmicutes;__Clostridia;__Clostridiales;__Lachnospiraceae;__g
EU5056 79	11.41789 6	0.003316 16	0.052582 72	5	0	6.8333333 3	Bacteria;__Firmicutes;__Clostridia;__Clostridiales;__Lachnospiraceae;__g
EF09633 7	11.29394 53	0.003528 18	0.052582 72	7.75	7.33333333	0	Bacteria;__Firmicutes;__Clostridia;__Clostridiales;__Lachnospiraceae;__g
EU4742 50	11.20098 04	0.003696 05	0.052582 72	2	0	0.3333333 3	Bacteria;__Firmicutes;__Clostridia;__Clostridiales;__Lachnospiraceae;__g
EU5055 40	10.95008 05	0.004190 06	0.052582 72	2	0	4	Bacteria;__Firmicutes;__Clostridia;__Clostridiales;__Lachnospiraceae;__g
DQ0148 15	10.89324 62	0.004310 84	0.052582 72	0	3	0	Bacteria;__Firmicutes;__Clostridia;__Clostridiales;__Lachnospiraceae;__g
EU5098 07	10.86956 52	0.004362 18	0.052582 72	0	34	0	Bacteria;__Firmicutes;__Clostridia;__Clostridiales;__Lachnospiraceae;__g

JQ08386	10.86956	0.004362	0.052582	0	100.166667	0	Bacteria; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; g
AY9911	10.86956	0.004362	0.052582	0	0	11.833333	Bacteria; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; g
EU5102	10.25316	0.005936	0.064127	8.5	0	0	Bacteria; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; g
EU5116	10.25316	0.005936	0.064127	6	0	0	Bacteria; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; g
DQ0147	9.674124	0.007930	0.078241	7.5	1	0	Bacteria; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; g
EU5053	9.579402	0.008314	0.079531	2.75	0.16666667	5.3333333	Bacteria; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; g
EU4744	9.493243	0.008680	0.081173	21.25	3.83333333	1.8333333	Bacteria; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; g
EU5100	9.361252	0.009273	0.084198	1.25	0	2.6666666	Bacteria; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; g
EU4549	9.280155	0.009656	0.085003	0.25	7.83333333	0	Bacteria; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; g
EU4742	9.141965	0.010347	0.085003	24	8.66666667	0.3333333	Bacteria; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; g
HQ7402	9.089003	0.010625	0.085894	0.25	0	1.3333333	Bacteria; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; g
EU5096	9.035539	0.010913	0.086546	0.25	4.16666667	0	Bacteria; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; g
EU5099	14.76923	0.000620	0.050162	3	0	0	Bacteria; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Incertae_Sedis
EU4554	10.91473	0.004264	0.052582	1.5	2.83333333	0	Bacteria; Firmicutes; Clostridia; Clostridiales; Lachnospiraceae; Incertae_Sedis
AY9911	14.65648	0.000656	0.050162	6.75	0	0	Bacteria; Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; g
EU5037	11.73705	0.002827	0.052582	0.75	2	0	Bacteria; Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; g
EF40669	11.06623	0.003953	0.052582	0	0.66666667	7.1666666	Bacteria; Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; g
EU4676	10.98367	0.004120	0.052582	0	2.16666667	11.1666666	Bacteria; Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; g
EU5100	10.92857	0.004235	0.052582	1.5	0	8.8333333	Bacteria; Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; g
EU5063	9.607247	0.008199	0.079424	0.25	3.83333333	0	Bacteria; Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; g
EU5052	9.125	0.010435	0.085003	2	3	0.1666666	Bacteria; Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; g
FJ68083	9.122807	0.010447	0.085003	0	2.83333333	0.1666666	Bacteria; Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; g
AY9937	14.00779	0.000908	0.050162	0	0	7.1666666	Bacteria; Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Incertae_Sedis
EU5073	10.96491	0.004159	0.052582	0	0	1.3333333	Bacteria; Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Incertae_Sedis
EF60378	10.89324	0.004310	0.052582	0	0	4	Bacteria; Firmicutes; Clostridia; Clostridiales; Ruminococcaceae; Incertae_Sedis

1	62	84	72				
EF09850 9	10.03095 98	0.006634 45	0.070256 08	8.5	2.16666667 3	0.3333333 3	Bacteria;__Firmicutes;__Clostridia;__Clostridiales;__Ruminococcaceae;__Incultae_Sedis
EF09664 0	9.175781 25	0.010174 3	0.085003 73	0.75	15.1666667	0.5	Bacteria;__Firmicutes;__Clostridia;__Clostridiales;__Ruminococcaceae;__Oscillibacter
EU4570 75	10.98901 1	0.004109 29	0.052582 72	0	1.1666666 7	0	Bacteria;__Firmicutes;__Clostridia;__Clostridiales;__uncultured;__g
DQ8157 99	11.75806 45	0.002797 49	0.052582 72	1.75	10.166666 7	0	Bacteria;__Firmicutes;__Erysipelotrichi;__Erysipelotrichales;__Erysipelotrichaceae;__g
JQ08385 9	11.72881 36	0.002838 71	0.052582 72	0.75	5	0	Bacteria;__Firmicutes;__Erysipelotrichi;__Erysipelotrichales;__Erysipelotrichaceae;__g
AB6064 07	11.02415 03	0.004037 72	0.052582 72	0	0.83333333 7	0	Bacteria;__Firmicutes;__Erysipelotrichi;__Erysipelotrichales;__Erysipelotrichaceae;__g
EU5082 51	9.713191 33	0.007776 91	0.077955 79	9	5.66666667 3	36.833333 3	Bacteria;__Firmicutes;__Erysipelotrichi;__Erysipelotrichales;__Erysipelotrichaceae;__g
AM9326 29	9.473241 02	0.008768 23	0.081382 15	10	6.33333333 35.5	0	Bacteria;__Firmicutes;__Erysipelotrichi;__Erysipelotrichales;__Erysipelotrichaceae;__Inculta_e_Sedis
AM9326 46	10.86956 52	0.004362 18	0.052582 72	0	12.6666667 0	0	Bacteria;__Proteobacteria;__Deltaproteobacteria;__Desulfovibrionales;__Desulfovibrionaceae;__Desulfovibrio
EU4572 32	10.43993 23	0.005407 51	0.062161 58	0	3.33333333 0.5	0	Bacteria;__Proteobacteria;__Deltaproteobacteria;__Desulfovibrionales;__Desulfovibrionaceae;__Desulfovibrio
AY9900 42	14.00778 21	0.000908 34	0.050162 4	0	0	25.166666 7	Bacteria;__Proteobacteria;__Epsilonproteobacteria;__Campylobacterales;__Helicobacteraceae;__Helicobacter
AM9326 39	10.52545 16	0.005181 16	0.060111 08	1.25	2	0	Bacteria;__Tenericutes;__Mollicutes;__Anaeroplasmatales;__Anaeroplasmataceae;__Anaeroplasma
EU9394 05	11.24031 01	0.003624 08	0.052582 72	38	0	54.166666 7	Bacteria;__Verrucomicrobia;__Verrucomicrobiae;__Verrucomicrobiales;__Verrucomicrobiaceae;__Akkermansia
DQ8053 03	11.24031 01	0.003624 08	0.052582 72	86	0	122.666666 7	Bacteria;__Verrucomicrobia;__Verrucomicrobiae;__Verrucomicrobiales;__Verrucomicrobiaceae;__Akkermansia
EU5074 86	9.541666 67	0.008473 32	0.080432 31	1	0	1.3333333 3	Bacteria;__Verrucomicrobia;__Verrucomicrobiae;__Verrucomicrobiales;__Verrucomicrobiaceae;__Akkermansia
EU7750 14	9.449476 65	0.008873 04	0.081749 36	3.25	0	3.5	Bacteria;__Verrucomicrobia;__Verrucomicrobiae;__Verrucomicrobiales;__Verrucomicrobiaceae;__Akkermansia

*Graphically represented in Supplementary Figure 2e.

Supplementary Table 5. Pathology H2 Congenics (Figure 2e-h) Significant differences by OTU*

OTU	Test-	P	FDR_P	BB	DD	KK		taxonomy
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	Statisti c			me an	me an	me an	
New.CleanUp.ReferenceO TU1285	9.91150 442	0.00704 278	0.07089 587	3	0	0	k_Bacteria
228798	9.85185 185	0.00725 6	0.07089 587	10	0	12. 2	k_Bacteria
1571092	9.48158 845	0.00873 171	0.07089 587	17	0.4	30. 4	k_Bacteria
3176547	7.64155 844	0.02191 072	0.09530 27	10. 8	0.6	41. 6	k_Bacteria
New.CleanUp.ReferenceO TU134143	13.29111 392	0.00129 977	0.07089 587	0	0	6.4	k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Bifidobacteriales;f_Bifidobacteriaceae;g_Bifidobacterium
681370	11.03522 941	0.00401 528	0.07089 587	0.2	1.2	106	k_Bacteria;p_Actinobacteria;c_Actinobacteria;o_Bifidobacteriales;f_Bifidobacteriaceae;g_Bifidobacterium;s_pseudolongum
New.CleanUp.ReferenceO TU212230	8.32182 741	0.01559 33	0.08141 434	2.6	0	0.2	k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales
New.ReferenceOTU969	7.65726 316	0.02173 934	0.09512 074	0	15	1	k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales
New.ReferenceOTU467	7.54328 358	0.02301 425	0.09791 994	0.4	9.6	2.6	k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales
New.CleanUp.ReferenceO TU120492	11.0518 248	0.00398 223	0.07089 587	0.6	25. 4	4.6	k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Bactero ides
181719	10.1030 411	0.00639 959	0.07089 587	8.6	177 .6	44	k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Bactero ides;s_
162539	13.2911 392	0.00129 977	0.07089 587	0	0	15. 4	k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae
New.ReferenceOTU1402	7.75555 556	0.02069 677	0.09263 873	0	3.6	22. 2	k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae;g_Rikenella :s_
215897	13.2911 392	0.00129 977	0.07089 587	8.4	0	0	k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_S24-7;g_;s_
New.CleanUp.ReferenceO TU76772	11.7050 228	0.00287 268	0.07089 587	3.2	0.2	0	k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_S24-7;g_;s_
New.ReferenceOTU190	11.6783 599	0.00291 123	0.07089 587	12	0	0.2	k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_S24-7;g_;s_
New.ReferenceOTU736	11.0526 316	0.00398 063	0.07089 587	16. 6	0.2	0.2	k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_S24-7;g_;s_
162025	10.4671 48	0.00533 443	0.07089 587	82. 2	0.4	11	k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_S24-7;g_;s_
261350	10.0606 526	0.00653 668	0.07089 587	76. 4	1.6	0.2	k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_S24-7;g_;s_
174805	9.91150 442	0.00704 278	0.07089 587	4	0	0	k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_S24-7;g_;s_
177533	9.91150 442	0.00704 278	0.07089 587	7.8	0	0	k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_S24-7;g_;s_
New.ReferenceOTU1265	9.91150 442	0.00704 278	0.07089 587	6.6	0	0	k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_S24-7;g_;s_
New.ReferenceOTU1677	9.91150 442	0.00704 278	0.07089 587	2	0	0	k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_S24-7;g_;s_
New.ReferenceOTU1642	9.91150	0.00704	0.07089	4	0	0	k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_S24-7;g_;s_

	442	278	587				
New.ReferenceOTU1144	9.91150 442	0.00704 278	0.07089 587	4.4	0	0	k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_S24-7;g_;
New.ReferenceOTU1526	9.88235 294	0.00714 619	0.07089 587	6.6	0	0	k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_S24-7;g_;
New.CleanUp.ReferenceOTU206210	9.88235 294	0.00714 619	0.07089 587	6.8	0	0	k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_S24-7;g_;
2212505	9.84179 104	0.00729 26	0.07089 .8	158	1.6	0.8	k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_S24-7;g_;
New.ReferenceOTU519	8.89113 924	0.01173 042	0.07676 224	1.4	15. 6	4	k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_S24-7;g_;
208434	8.72230 216	0.01276 369	0.07847 564	38. 2	111	31. 6	k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_S24-7;g_;
2435303	8.30075 949	0.01575 843	0.08141 434	17. 8	0.2	0	k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_S24-7;g_;
New.ReferenceOTU627	8.30075 949	0.01575 843	0.08141 434	6.2	0	0.2	k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_S24-7;g_;
New.ReferenceOTU63	8.12954 545	0.01716 689	0.08431 842	8.2	1.8	0.2	k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_S24-7;g_;
New.CleanUp.ReferenceOTU90984	7.65524 297	0.02176 131	0.09512 074	0	1.4	0.2	k_Bacteria;p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_S24-7;g_;
New.ReferenceOTU685	8.98074 074	0.01121 649	0.07560 995	0.8	14	2	k_Bacteria;p_Firmicutes
418334	8.16443 595	0.01687 001	0.08390 017	4.8	0	4.8	k_Bacteria;p_Firmicutes
637934	7.51832 061	0.02330 33	0.09877 421	13. 8	0.4	31. 6	k_Bacteria;p_Firmicutes
318764	10.4437 956	0.00539 708	0.07089 587	0.8	12. 6	1.6	k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus
509149	9.45393 258	0.00885 329	0.07089 587	1.2	7.2	0.6	k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus
New.ReferenceOTU1373	7.70126 582	0.02126 627	0.09405 913	3.2	12. 8	3.2	k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus
4397402	10.3610 687	0.00562 5	0.07089 587	2.4	184. .4	1.4	k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus; s_
4428313	9.56834 532	0.00836 104	0.07089 587	81. 4	1.4	54. 2	k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus; s_
New.ReferenceOTU1518	11.4704 545	0.00323 015	0.07089 587	0.6	8.2	2.6	k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus; s_vaginalis
New.ReferenceOTU962	9.19064 748	0.01009 895	0.07141 835	5.2	23. 8	9.4	k_Bacteria;p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus; s_vaginalis
214919	10.2809 16	0.00585 501	0.07089 587	1	1	62. 6	k_Bacteria;p_Firmicutes;c_Bacilli;o_Turicibacteriales;f_Turicibacteraceae;g_Turicibacter s_
234912	13.3248 731	0.00127 803	0.07089 587	0	0	8.4	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
195711	13.2911 392	0.00129 977	0.07089 587	0	0	41	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
260156	12.1184 51	0.00233 621	0.07089 587	0.4	0	9.6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales

293754	12.0909 091	0.00236 86	0.07089 587	0	0.2	15. 6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
337407	11.7050 228	0.00287 268	0.07089 587	0.2	0	6.6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
215018	11.6898 608	0.00289 454	0.07089 587	1	0	11. 4	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
261590	11.6176 471	0.00300 096	0.07089 587	0.6	0	128. .4	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
New.ReferenceOTU717	11.5087 85	0.00316 883	0.07089 587	1.8	0.6	13. 6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
New.CleanUp.ReferenceO TU137408	11.2254 545	0.00365 11	0.07089 587	1.6	9.6	0	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
New.ReferenceOTU1426	11.2051 376	0.00368 838	0.07089 587	3.4	0.2	12. 2	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
174824	11.1596 396	0.00377 325	0.07089 587	69. 8	361. .6	1.2	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
635059	11.0759 494	0.00393 449	0.07089 587	0.2	0.2	9.8	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
New.ReferenceOTU760	10.9724 008	0.00414 356	0.07089 587	1.2	0.2	7.4	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
322564	10.8091 778	0.00449 59	0.07089 587	3.8	0.2	48. 8	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
New.ReferenceOTU64	10.7493 562	0.00463 241	0.07089 587	4	0	0.8	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
New.ReferenceOTU802	10.6664 151	0.00482 856	0.07089 587	2	0	3	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
275138	10.64	0.00489 275	0.07089 587	0.2	0.4	12. 8	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
173939	10.4429 423	0.00539 938	0.07089 587	2.6	0	15. 8	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
307170	10.3120 721	0.00576 45	0.07089 587	17. 4	0.6	32	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
195433	10.2809 16	0.00585 501	0.07089 587	0.6	1	22. 2	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
335632	10.2726 115	0.00587 937	0.07089 587	6	0.2	0.2	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
New.ReferenceOTU31	10.2305 709	0.00600 426	0.07089 587	2.8	0.2	4.8	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
New.ReferenceOTU1331	10.08	0.00647 375	0.07089 587	1.4	7.8	0.2	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
162576	10.0768 362	0.00648 4	0.07089 587	0	9	6.6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
198537	9.88235 294	0.00714 619	0.07089 587	0	0	3.2	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
227967	9.88235 294	0.00714 619	0.07089 587	0	0	18. .2	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
335183	9.88015 267	0.00715 405	0.07089 587	4.6	0.6	83. .8	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
New.ReferenceOTU280	9.83376	0.00732	0.07089	14.	0.2	41.	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales

	623	192	587	8		6	
176486	9.79701 493	0.00745 771	0.07089 587	0	0.6	9.4	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
175758	9.75942 029	0.00759 922	0.07089 587	2.8	3	271 .6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
189024	9.72740 741	0.00772 183	0.07089 587	9.2	1.8	31. 2	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
202419	9.58133 874	0.00830 69	0.07089 587	0.2	0.4	12. 2	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
174698	9.57435 897	0.00833 594	0.07089 587	0.8	1.8	15. 6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
180944	9.55458 167	0.00841 878	0.07089 587	1	0.2	8	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
New.ReferenceOTU1671	9.45325 885	0.00885 627	0.07089 587	1	0.8	6.6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
179703	9.42558 14	0.00897 968	0.07089 587	0.8	0.4	4.6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
332854	9.40446 097	0.00907 501	0.07089 587	5.4	15	0.2	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
313724	9.38527 828	0.00916 247	0.07089 587	18. 6	3	6.6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
190063	9.35555 556	0.00929 966	0.07127 614	4.8	0	11. 4	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
263899	9.32738 854	0.00943 156	0.07133 005	1	0	4.4	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
New.ReferenceOTU1117	9.32661 871	0.00943 519	0.07133 005	10	3.2	21	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
264359	9.29451 796	0.00958 785	0.07133 005	0.6	4.4	1.4	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
180919	9.25659 656	0.00977 137	0.07133 005	2	0.2	6.8	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
New.ReferenceOTU1324	9.24848 485	0.00981 108	0.07133 005	0.6	3.2	0.8	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
New.CleanUp.ReferenceO TU85373	9.15605 214	0.01027 516	0.07141 835	1.8	0.4	7	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
New.CleanUp.ReferenceO TU36979	9.06581 741	0.01074 936	0.07355 839	0.4	5.4	0.2	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
356353	8.92403 67	0.01153 905	0.07595 41	2.2	1.2	28. 4	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
4364242	8.83976 143	0.01203 567	0.07730 68	0.4	3	46. 2	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
New.ReferenceOTU1270	8.74479 83	0.01262 092	0.07846 008	2	0	6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
4364243	8.68946 322	0.01297 499	0.07848 116	10. 2	0	27	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
271734	8.63805 668	0.01331 281	0.07923 956	1.2	0	2.4	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
267411	8.61818 182	0.01344 577	0.07936 454	10	0.2	31	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales

267752	8.45017 921	0.01462 402	0.08141 434	31	77. 4	13. 6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
198363	8.42058 824	0.01484 2	0.08141 434	0.4	3.2	4	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
346291	8.4	0.01499 558	0.08141 434	33. 4	16. 6	0	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
New.ReferenceOTU484	8.4	0.01499 558	0.08141 434	19. 4	0	26. 2	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
229452	8.30289 017	0.01574 165	0.08141 434	7.2	0	4.8	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
New.CleanUp.ReferenceO TU151457	8.29157 175	0.01583 099	0.08141 434	4.8	0	5.2	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
199731	8.27891 892	0.01593 146	0.08141 434	87	1.2	146. .2	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
318819	8.27272 727	0.01598 086	0.08141 434	3.4	8.6	0	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
274289	8.22366 412	0.01637 774	0.08292 621	8.2	0	7.2	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
771177	8.18461 538	0.01670 065	0.08342 869	28	0.4	28. 4	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
195885	8.08230 769	0.01757 718	0.08551 68	1.2	0.2	5.2	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
New.ReferenceOTU136	7.99198 543	0.01838 918	0.08756 381	5.8	0.8	10. 2	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
268379	7.97251 908	0.01856 904	0.08804 558	0.2	0	6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
172464	7.92442 748	0.01902 096	0.08905 629	4.6	0.2	10. 4	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
199674	7.86113 208	0.01963 256	0.09115 697	5.2	0.6	30. 4	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
New.ReferenceOTU554	7.81550 696	0.02008 557	0.09225 034	1.8	8	0.4	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
317389	7.81518 987	0.02008 876	0.09225 034	0.6	0.6	8.8	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
185923	7.77910 448	0.02045 45	0.09263 873	0.2	0.4	4.6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
260346	7.76202 532	0.02062 992	0.09263 873	8	26. 4	6.4	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
134065	7.66315 789	0.02167 536	0.09512 074	1.8	0.8	6.8	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
New.ReferenceOTU1007	7.54805 195	0.02295 944	0.09791 994	25. 2	0.2	11	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales
264660	13.2911 392	0.00129 977	0.07089 587	0	13	0	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_g_s
259870	12.1184 51	0.00233 621	0.07089 587	0.2	0	16. 6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_g_s
174126	12.0909 091	0.00236 86	0.07089 587	0	0.2	10. 4	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_g_s
349874	12.0909	0.00236	0.07089	1.2	0	19	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_g_s

	091	86	587				
259820	12.0909 091	0.00236 86	0.07089 587	0.8	0	38. 6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
New.CleanUp.ReferenceOTU14730	11.6783 599	0.00291 123	0.07089 587	0.4	0	7.6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
268063	11.4446 097	0.00327 216	0.07089 587	6.4	0	11. 6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
New.ReferenceOTU1136	11.2254 545	0.00365 11	0.07089 587	2	25. 8	0	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
New.ReferenceOTU995	10.9336 032	0.00422 472	0.07089 587	1.8	0	7.2	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
268492	10.9013 333	0.00429 344	0.07089 587	4.2	0.4	32	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
New.ReferenceOTU549	10.6464 491	0.00487 7	0.07089 587	2.2	0	7.4	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
1108453	10.6282 105	0.00492 168	0.07089 587	22. 4	0.4	0.2	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
330296	10.4346 241	0.00542 188	0.07089 587	0.8	0	16. 4	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
New.ReferenceOTU420	10.2404 81	0.00597 459	0.07089 587	0.8	0	4.2	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
228043	10.1560 229	0.00623 229	0.07089 587	4.8	0.2	22. 2	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
185177	10.1187 614	0.00634 949	0.07089 587	60. 2	0.4	107. .6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
351309	10.1003 636	0.00640 817	0.07089 587	114. .2	0.6	213. .8	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
197706	10.0728 597	0.00649 69	0.07089 587	28. 4	0.6	43	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
272455	10.0213 333	0.00666 646	0.07089 587	6.8	1.2	73. .4	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
275618	9.97595 628	0.00681 944	0.07089 587	28. 2	1.2	139. .8	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
191811	9.96328 872	0.00686 277	0.07089 587	7.2	0	17. .4	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
197568	9.96183 486	0.00686 776	0.07089 587	2.2	38	1.4	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
317653	9.95781 818	0.00688 157	0.07089 587	16. 8	0.4	22. .2	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
272092	9.94427 481	0.00692 832	0.07089 587	15. .4	0	30. .6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
272619	9.91150 442	0.00704 278	0.07089 587	0	0	7.6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
275796	9.90597 61	0.00706 227	0.07089 587	1.4	0	5.6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
New.ReferenceOTU1039	9.82692 308	0.00734 701	0.07089 587	8.4	0	14	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
189585	9.75190 84	0.00762 781	0.07089 587	31. .6	0	41. .2	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__

267124	9.67272 727	0.00793 586	0.07089 587	16. 2	0.4	21. 8	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
New.ReferenceOTU858	9.66307 385	0.00797 426	0.07089 587	1.2	0	4.2	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
258165	9.64135 189	0.00806 134	0.07089 587	0.4	0.6	35. 4	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
3919792	9.54018 018	0.00847 962	0.07089 587	9	109. .6	9.2	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
182712	9.47653 43	0.00875 38	0.07089 587	30. 2	0.4	23	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
196697	9.45719 626	0.00883 885	0.07089 587	2.2	5	0.2	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
3868285	9.408	0.00905 897	0.07089 587	1.2	0.2	19. 6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
193288	9.26666 667	0.00972 23	0.07133 005	1.6	0.2	11. .6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
262556	9.24663 024	0.00982 019	0.07133 005	65	0.6	44. 2	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
267914	9.24312 268	0.00983 742	0.07133 005	27. 8	0.2	37. 4	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
184451	9.20888 889	0.01000 726	0.07133 005	141	0.6	252. .4	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
New.ReferenceOTU402	9.20876 494	0.01000 788	0.07133 005	1.2	0.2	8.8	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
258812	9.14358 974	0.01033 939	0.07141 835	8.8	0.6	40. 4	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
New.ReferenceOTU1364	9.01923 077	0.01100 269	0.07461 825	2	0	4.6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
New.ReferenceOTU934	8.95551 102	0.01135 888	0.07571 145	1	8.4	0.4	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
New.ReferenceOTU463	8.95410 526	0.01136 687	0.07571 145	1.2	0	4.8	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
New.CleanUp.ReferenceOTU141476	8.87392 996	0.01183 179	0.07697 545	1.8	0	4.4	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
298723	8.83767 535	0.01204 823	0.07730 68	0.6	0.2	4	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
New.ReferenceOTU408	8.79676 113	0.01229 724	0.07730 68	2	0.2	3.6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
New.ReferenceOTU1383	8.75062 612	0.01258 42	0.07846 008	6.8	23. .4	10. .2	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
New.ReferenceOTU1717	8.69112	0.01296 373	0.07848 116	1.6	0.2	6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
276580	8.65036 496	0.01323 114	0.07917 455	9.6	0.4	13. .2	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
271219	8.60322 581	0.01354 669	0.07936 517	1	0	3.4	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
179265	8.57060 932	0.01376 943	0.08024 994	29. .8	5.6	83. .2	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
New.ReferenceOTU1573	8.5344	0.01402	0.08129	4.4	0	7.2	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__

		099	267				
271403		8.38235 294	0.01512 848	0.08141 434	2.4	0	5.8 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
196571		8.38235 294	0.01512 848	0.08141 434	5.8	0	13. 4 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
329528		8.30075 949	0.01575 843	0.08141 434	0	0.2	5.4 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
New.ReferenceOTU803		8.29157 175	0.01583 099	0.08141 434	1.6	0	2.6 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
176298		8.28458 781	0.01588 637	0.08141 434	162	3.2	206. .8 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
276762		8.27272 727	0.01598 086	0.08141 434	4.8	0	4 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
New.ReferenceOTU543		8.0864	0.01754 125	0.08551 68	2.2	0.4	6.4 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
4424327		8.00512 821	0.01826 874	0.08756 381	59. 2	0.6	169 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
New.ReferenceOTU287		7.96008 493	0.01868 485	0.08822 085	1.8	0	3 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
1112121		7.93705 179	0.01890 128	0.08886 776	2	0.2	10. 6 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
266091		7.90557 621	0.01920 109	0.08952 509	7.2	0.2	16. .2 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
New.ReferenceOTU845		7.80655 106	0.02017 572	0.09225 034	2	0.2	4.6 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
274374		7.78015 267	0.02044 379	0.09263 873	12. 2	0.4	20 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
271494		7.72987 013	0.02096 428	0.09346 228	1.4	13. 4	2.4 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__;g__;s__
2797565		11.0301 471	0.00402 563	0.07089 587	2.8	0.2	5.8 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__[Mogibacteriaceae];g__;s__
228140		7.76168 582	0.02063 343	0.09263 873	2.6	10. 2	0.2 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__[Mogibacteriaceae];g__;s__
4383953		13.2911 392	0.00129 977	0.07089 587	0	0	96. .8 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__Clostridiaceae;g__Clostridium
189407		13.2911 392	0.00129 977	0.07089 587	0	0	88. .2 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__Clostridiaceae;g__SMB53;s__
196315		12.0909 091	0.00236 86	0.07089 587	0.2	0	24 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__Clostridiaceae;g__SMB53;s__
347908		13.3248 731	0.00127 803	0.07089 587	0	0	11. .2 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__Lachnospiraceae
3392840		12.1184 51	0.00233 621	0.07089 587	0.2	0	13. .6 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__Lachnospiraceae
305750		11.6783 599	0.00291 123	0.07089 587	0.2	0	4.6 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__Lachnospiraceae
320912		10.8993 684	0.00429 766	0.07089 587	3.4	25. .6	0 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__Lachnospiraceae
203970		10.6781 362	0.00480 034	0.07089 587	93. .4	16. .2	239 k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f__Lachnospiraceae

273376	10.4346 241	0.00542 188	0.07089 587	2.8	0	0.4	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae
New.ReferenceOTU1674	10.4346 241	0.00542 188	0.07089 587	1	0	13	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae
2120784	9.92727 273	0.00698 747	0.07089 587	4.4	1	76. 6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae
38415	9.89266 547	0.00710 943	0.07089 587	12. 2	60. 8	15. 8	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae
264345	9.66924 829	0.00794 968	0.07089 587	14	76. 6	0	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae
4393892	9.63720 93	0.00807 805	0.07089 587	153	40. .8	49. 2	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae
New.ReferenceOTU185	8.80145 191	0.01226 843	0.07730 68	6	1	5.4	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae
1991255	8.65501 859	0.01320 038	0.07917 455	3.4	0.2	3	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae
190425	8.4	0.01499 558	0.08141 434	5.6	3.6	1	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae
747987	8.30075 949	0.01575 843	0.08141 434	0	0.2	7.2	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae
4418586	8.30075 949	0.01575 843	0.08141 434	0	0.2	18. 6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae
277497	8.02599 278	0.01807 914	0.08736 524	1.6	12. .8	8.6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae
180800	10.0914 498	0.00643 679	0.07089 587	13. 6	0.6	77. 2	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_s
193680	9.71234 347	0.00778 021	0.07089 587	30	18. .4	2.8	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_s
258522	9.58054 054	0.00831 021	0.07089 587	74. 2	2.6	210	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_s
172161	9.38823 529	0.00914 894	0.07089 587	1.6	0.2	21. .4	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_s
266192	9.38	0.00918 669	0.07089 587	37	96. 8	55. .8	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_s
180105	8.93454 545	0.01147 858	0.07595 41	3.2	0	19. .4	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_s
273091	8.61374 046	0.01347 566	0.07936 454	5.4	0.6	40. .2	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_s
327739	8.30075 949	0.01575 843	0.08141 434	8	0	0.2	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_s
188078	8.30075 949	0.01575 843	0.08141 434	34. .4	0.2	0	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_s
186052	8.26953 405	0.01600 639	0.08141 434	22. .4	11. .6	7.4	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_s
261114	8.18778 947	0.01667 417	0.08342 869	1.4	0.4	17. .2	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_s
2611178	8.02222 222	0.01811 326	0.08736 524	17. .8	0.2	60. .8	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_s
346648	7.54671	0.02297	0.09791	12	7	0.8	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_s

	533	479	994				
3750373	12.5899 281	0.00184 558	0.07089 587	2.6	31. 6	9	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_[Ruminococc us];s_gnavus
262537	10.6520 646	0.00486 333	0.07089 587	5.2	25. 2	14. 8	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_[Ruminococc us];s_gnavus
2897332	9.15109 489	0.01030 066	0.07141 835	8.6	1.8	6.2	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_[Ruminococc us];s_gnavus
266726	12.0909 091	0.00236 86	0.07089 587	0.2	0	10	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Coprococcus
182016	11.3284 404	0.00346 785	0.07089 587	0.2	0	4.6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Coprococcus; s;s_
262227	8.32182 741	0.01559 33	0.08141 434	0.4	0	6.6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Coprococcus; s;s_
309480	10.0157 706	0.00668 503	0.07089 587	6.2	39. 8	8.2	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Dorea
192204	9.06	0.01078 068	0.07355 839	23. 8	108	36. 6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Dorea
193509	8.70677 291	0.01286 318	0.07848 116	3.2	0	7.6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Dorea
170185	9.91150 442	0.00704 278	0.07089 587	2.2	0	0	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae
389529	9.66242 775	0.00797 683	0.07089 587	3.8	0	1.6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae
199307	9.64444 444	0.00804 888	0.07089 587	11. 8	0.2	7	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae
344906	9.58540 146	0.00829 004	0.07089 587	10	0.2	9.4	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae
177271	8.4	0.01499 558	0.08141 434	8.4	0	7	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae
273586	8.12954 545	0.01716 689	0.08431 842	1.6	0.2	3.8	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae
375106	8.128	0.01718 016	0.08431 842	4	0.2	10	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae
New.ReferenceOTU617	7.63585 657	0.02197 328	0.09530 27	3.4	0	3.8	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae
192598	8.27272 727	0.01598 086	0.08141 434	8.2	0	13	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_s_
180879	12.6126 126	0.00182 476	0.07089 587	34	1.4	13. 8	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Oscillospira s_
356055	11.7131 474	0.00286 103	0.07089 587	1	0	5.4	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Oscillospira s_
166226	11.6783 599	0.00291 123	0.07089 587	0.2	14. 8	0	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Oscillospira s_
267689	11.0344 086	0.00401 706	0.07089 587	21. 8	5.2	86. 6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Oscillospira s_
178959	10.8978 417	0.00430 094	0.07089 587	24. 6	2	52	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Oscillospira s_
New.ReferenceOTU9	10.8219 178	0.00446 735	0.07089 587	0.6	0.2	3	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Oscillospira s_

307608	10.4222 222	0.00545 561	0.07089 587	1.8	13. 4	31. 6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Oscillospira ;s_
1110253	10.3728 44	0.00559 198	0.07089 587	2.2	0.6	15. 6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Oscillospira ;s_
265793	9.89184 891	0.00711 234	0.07089 587	1	0.2	10	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Oscillospira ;s_
275423	9.67970 75	0.00790 821	0.07089 587	2.2	1	115	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Oscillospira ;s_
167034	9.50592 46	0.00862 61	0.07089 587	22. 6	5	27. 6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Oscillospira ;s_
332608	9.41909 91	0.00900 883	0.07089 587	1	7.6	5	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Oscillospira ;s_
180235	9.23116 883	0.00989 64	0.07133 005	2	12. 4	0.8	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Oscillospira ;s_
165046	9.14936 709	0.01030 956	0.07141 835	17. 6	0.8	32. 6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Oscillospira ;s_
191558	8.80218 182	0.01226 395	0.07730 68	9.8	9	17. 4	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Oscillospira ;s_
273648	8.72288 288	0.01275 998	0.07847 564	13. 2	0.8	15. 4	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Oscillospira ;s_
180535	8.48220 183	0.01439 174	0.08141 434	2.2	0.6	9.2	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Oscillospira ;s_
832558	8.20726 577	0.01651 258	0.08323 232	4.2	0.4	14. 6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Oscillospira ;s_
275543	7.99922 631	0.01832 273	0.08756 381	1.2	0.4	5.6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Oscillospira ;s_
304080	7.80436 364	0.02019 78	0.09225 034	5.6	1.2	10. 6	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Oscillospira ;s_
258725	7.70133 333	0.02126 555	0.09405 913	14. 8	0.2	36	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Oscillospira ;s_
189840	7.59355 993	0.02244 292	0.09696 382	21. 4	26. 8	170	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Oscillospira ;s_
194662	7.55443 038	0.02288 634	0.09791 994	6.6	2.2	13. 4	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Oscillospira ;s_
261365	10.2788 104	0.00586 117	0.07089 587	5.2	0	10. 8	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Ruminococ cus;s_
268720	9.38	0.00918 669	0.07089 587	31. 2	44. 4	14. 4	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Ruminococ cus;s_
189147	8.82960 289	0.01209 696	0.07730 68	19	0.6	20	k_Bacteria;p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Ruminococ cus;s_

*Graphically represented in Supplementary Figure 2e

Supplementary Table 6. Biology H2 Congenics (Figure 2i-l) Significant differences by OTU*

OTU	Test-Statistic	P	FDR_P	BB_mean	DD_mean	KK_mean	taxonomy
EF097218	8.97795591	0.01123212	0.08788206	1.8	0	3.8	Bacteria; __Actinobacteria; __Coriobacteriia; __Coriobacteriales; __Coriobacteriaceae; __Enterorhabdus
DQ014947	13.2911392	0.00129977	0.04406832	22	0	0	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __Porphyromonadaceae; __Barnesiella
EF614623	12.962963	0.00153154	0.0464024	274.2	0	698.2	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __Prevotellaceae; __g
EF096895	11.5207767	0.00314989	0.06579326	1.4	0	5.4	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __Prevotellaceae; __g

EU505099	13.0841121	0.00144152	0.0464024	5	0	14.4	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __Prevotellaceae; __Prevotella
DQ815668	13.3248731	0.00127803	0.04406832	5.2	0	0	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __Rikenellaceae; __Alistipes
AY991070	11.6176471	0.00300096	0.06579326	168	0	18.2	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __Rikenellaceae; __Alistipes
EU457823	11.3544828	0.00342299	0.06579326	2.8	0	0.2	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __Rikenellaceae; __Alistipes
EU655844	9.91150442	0.00704278	0.06579326	3.4	0	0	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __Rikenellaceae; __Alistipes
EF100034	8.82	0.01215518	0.09266714	16.8	79	70	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __Rikenellaceae; __Alistipes
EF406867	13.42711	0.00121434	0.04406832	2.4	0	0	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EU505154	13.3248731	0.00127803	0.04406832	36.8	0	0	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EF097510	13.3248731	0.00127803	0.04406832	4.8	0	0	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EU505465	13.3248731	0.00127803	0.04406832	7.2	0	0	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EF406803	13.3248731	0.00127803	0.04406832	11.8	0	0	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EF098040	13.2911392	0.00129977	0.04406832	6	0	0	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EU504810	13.2911392	0.00129977	0.04406832	19.2	0	0	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EU791170	13.2911392	0.00129977	0.04406832	56.4	0	0	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EU456778	13.2911392	0.00129977	0.04406832	73	0	0	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EU504432	13.2911392	0.00129977	0.04406832	30.8	0	0	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EF097526	13.2911392	0.00129977	0.04406832	10.6	0	0	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EU655810	13.2911392	0.00129977	0.04406832	56.4	0	0	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EF099648	13.2911392	0.00129977	0.04406832	13.2	0	0	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EF097554	13.2911392	0.00129977	0.04406832	6.6	0	0	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EF406486	13.2911392	0.00129977	0.04406832	56.6	0	0	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EU510749	13.0841121	0.00144152	0.0464024	12.2	0	27	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EU453830	12.987013	0.00151323	0.0464024	5.4	0	25.6	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EU457245	12.962963	0.00153154	0.0464024	7	0	48.8	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EU452656	12.1797323	0.00226571	0.06579326	2	0	22.4	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7;

							—g
EF406569	12.0909091	0.0023686	0.06579326	13.4	0.2	0	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EU510625	11.6898608	0.00289454	0.06579326	11.8	0	75.4	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
AY990698	11.6783599	0.00291123	0.06579326	0.2	0	3.6	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EU504803	10.9686441	0.00415135	0.06579326	5.8	0	1.4	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EU503894	10.6181818	0.00494642	0.06579326	4.6	0	8.4	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EU504801	10.5291089	0.0051717	0.06579326	1	0	2.8	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EU504568	10.4463551	0.00539017	0.06579326	6.8	0	4.8	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EU504184	10.3413333	0.00568078	0.06579326	2.4	0	1.8	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EU505382	10.1818182	0.00615242	0.06579326	0.8	0	0	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EU452809	10	0.00673795	0.06579326	1.2	0	0	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EF097783	10	0.00673795	0.06579326	1	0	0	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EF096871	9.9408284	0.00694027	0.06579326	1.2	0	0	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EF406765	9.9408284	0.00694027	0.06579326	1.2	0	0	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EU457101	9.91150442	0.00704278	0.06579326	13.8	0	0	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EF406873	9.91150442	0.00704278	0.06579326	3.4	0	0	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EF406646	9.91150442	0.00704278	0.06579326	1.6	0	0	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EF096622	9.91150442	0.00704278	0.06579326	1.8	0	0	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EF614662	9.91150442	0.00704278	0.06579326	5.6	0	0	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EF406710	9.91150442	0.00704278	0.06579326	1.4	0	0	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EF406592	9.88235294	0.00714619	0.06579326	18.2	0	0	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EU503917	9.88235294	0.00714619	0.06579326	0	8.4	0	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EF406815	9.88235294	0.00714619	0.06579326	2	0	0	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EF098484	9.85243446	0.00725389	0.06579326	4.8	0	6	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EF099832	9.83770197	0.00730752	0.0658602	8.4	70.4	4	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g

EU455919	9.79490909	0.00746556	0.06670634	117.8	11.6	105	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EF099130	9.75742397	0.00760681	0.06686476	19.6	48.4	81.6	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EU504899	9.72740741	0.00772183	0.0670481	423.2	0	383.6	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EU455595	9.59127273	0.00826574	0.07018886	234.8	26	206.4	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EF406607	9.3996357	0.00909693	0.07575458	25.8	2.2	23.2	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EU455460	9.32008114	0.00946608	0.07791732	2.8	0	1	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EU458112	9.30569476	0.00953442	0.07801507	15	4.4	0	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EU507474	9.2765653	0.0096743	0.07815183	20.6	603.2	50.8	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EF406866	9.26835443	0.0097141	0.07815183	3.6	1	0	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EU504185	9.04373832	0.01086869	0.08598341	0.8	11.6	0.8	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EF099162	8.60400729	0.0135414	0.09991167	27.6	3.4	21	Bacteria; __Bacteroidetes; __Bacteroidia; __Bacteroidales; __S24-7; __g
EU509932	12.0909091	0.0023686	0.06579326	14	0	0.6	Bacteria; __Bacteroidetes; __VC2.1_Bac22; __o; __f; __g
DQ815839	13.2911392	0.00129977	0.04406832	0	0	56.8	Bacteria; __Candidate_division_TM7; __c; __o; __f; __g
HM124025	13.2911392	0.00129977	0.04406832	0	0	18.4	Bacteria; __Candidate_division_TM7; __c; __o; __f; __g
EF095966	13.2911392	0.00129977	0.04406832	0	0	23.8	Bacteria; __Candidate_division_TM7; __c; __o; __f; __g
AY991178	9.88235294	0.00714619	0.06579326	0	0	19.8	Bacteria; __Candidate_division_TM7; __c; __o; __f; __g
EU510641	13.3587786	0.00125655	0.04406832	0	0	6.2	Bacteria; __Firmicutes; __Bacilli; __Lactobacillales; __Lactobacillaceae; __Lactobacillus
EF096152	11.6898608	0.00289454	0.06579326	1	23	0	Bacteria; __Firmicutes; __Bacilli; __Lactobacillales; __Lactobacillaceae; __Lactobacillus
EU505198	10.6975701	0.00475392	0.06579326	4.4	0	10.8	Bacteria; __Firmicutes; __Bacilli; __Lactobacillales; __Lactobacillaceae; __Lactobacillus
EU505448	10.3496296	0.00565726	0.06579326	28.8	0	45.6	Bacteria; __Firmicutes; __Bacilli; __Lactobacillales; __Lactobacillaceae; __Lactobacillus
EU457074	9.88235294	0.00714619	0.06579326	0	142.8	0	Bacteria; __Firmicutes; __Bacilli; __Lactobacillales; __Lactobacillaceae; __Lactobacillus
EU451393	9.78701299	0.00749509	0.06670634	10.2	0	12.4	Bacteria; __Firmicutes; __Bacilli; __Lactobacillales; __Lactobacillaceae; __Lactobacillus
EU451013	9.76888889	0.00756332	0.06686476	26.4	0	34	Bacteria; __Firmicutes; __Bacilli; __Lactobacillales; __Lactobacillaceae; __Lactobacillus
EU761885	9.91150442	0.00704278	0.06579326	2.4	0	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Christensenellaceae; __Christensenella
EU469268	13.6363636	0.00109371	0.04406832	1.2	0	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Christensenellaceae; __g
EF099030	10	0.00673795	0.06579326	0	1.4	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Family XIII_Incertae_Sedis; __Incertae_Sedis

AY993664	9.91150442	0.00704278	0.06579326	0	0	1.8	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __Coprococcus
EU511743	9.88235294	0.00714619	0.06579326	49.6	0	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __Coprococcus
EU462089	10.1818182	0.00615242	0.06579326	0	0	0.8	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __Dorea
EU456889	13.42711	0.00121434	0.04406832	0	2.8	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EU503956	13.42711	0.00121434	0.04406832	1.6	0	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EU457789	13.3248731	0.00127803	0.04406832	0	0	2.4	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
DQ015528	13.3248731	0.00127803	0.04406832	0	2.8	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EU504205	13.2911392	0.00129977	0.04406832	44.8	0	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EU509990	13.2911392	0.00129977	0.04406832	6.2	0	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EU503953	13.2911392	0.00129977	0.04406832	47.4	0	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EU503995	13.2911392	0.00129977	0.04406832	63	0	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EU503881	13.2911392	0.00129977	0.04406832	26.6	0	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EU504214	13.2911392	0.00129977	0.04406832	6.6	0	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EU508368	12.0909091	0.0023686	0.06579326	1	42.2	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EU508707	11.9592308	0.0025298	0.06579326	1	9.2	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EU510102	11.7684211	0.00278304	0.06579326	3	10.2	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EU453073	11.3544828	0.00342299	0.06579326	0	3.4	0.4	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EU504233	11.3284404	0.00346785	0.06579326	0	0.2	4	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EU510378	11.0907063	0.00390556	0.06579326	4	0	15.2	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EU511776	11.0453333	0.00399518	0.06579326	3.8	0	13.4	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EU511760	10.9686441	0.00415135	0.06579326	16.8	0	0.4	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EU509071	10.9557809	0.00417813	0.06579326	1	0	15	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EU455386	10.8587814	0.00438577	0.06579326	1.6	8.6	18.8	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EU454243	10.7476923	0.00463627	0.06579326	0.2	0.8	28	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EU455488	10.6669231	0.00482733	0.06579326	1.2	8.4	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales;

							__Lachnospiraceae; __g
EU511991	10.5617647	0.00508794	0.06579326	0.4	2.2	5.2	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
AY990911	10.5056	0.00523285	0.06579326	4.4	0	0.8	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EF099230	10.3610687	0.005625	0.06579326	2.8	21.2	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EU505206	10.240481	0.00597459	0.06579326	0.8	5.2	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EU457662	10.1818182	0.00615242	0.06579326	0	0.8	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EU504592	10.1066667	0.006388	0.06579326	0.4	0	1.8	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
AM932651	10.0912409	0.00643747	0.06579326	3	1.6	43.6	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EU504066	10.0671756	0.00651539	0.06579326	0.6	1.4	33.2	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EU451636	10.0507463	0.00656913	0.06579326	4.4	0	5.6	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EU457126	10.0258065	0.00665156	0.06579326	0	1	4	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EU503625	10	0.00673795	0.06579326	1.2	0	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EU454538	9.9408284	0.00694027	0.06579326	0	1.6	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EU452997	9.91150442	0.00704278	0.06579326	0	1.6	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EU504224	9.91150442	0.00704278	0.06579326	1.4	0	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
GQ493732	9.91150442	0.00704278	0.06579326	0	0	1.6	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
AY992736	9.91150442	0.00704278	0.06579326	1.8	0	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EU503678	9.9059761	0.00706227	0.06579326	0	4	1.2	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EU505155	9.88235294	0.00714619	0.06579326	0	0	59.4	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EF098033	9.88235294	0.00714619	0.06579326	0	2.4	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EU504017	9.88235294	0.00714619	0.06579326	6.2	0	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EU507860	9.88235294	0.00714619	0.06579326	8.6	0	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EU503948	9.88235294	0.00714619	0.06579326	2.4	0	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EU457269	9.87368421	0.00717723	0.06579326	0	6.8	20	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EF096560	9.85263158	0.00725318	0.06579326	1.4	0.6	5	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g

EU509827	9.73284133	0.00770088	0.0670481	0.8	1	6.4	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EU507528	9.36266174	0.00926667	0.07671943	0.2	2.8	5.4	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EU504701	9.29458484	0.00958753	0.07801507	0.6	35.8	9	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EU505623	9.03208955	0.01093218	0.08600785	0.2	2.8	5.6	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EU511694	8.8648855	0.01188542	0.09198282	13.2	0.2	5.6	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EU510606	8.84756335	0.01198881	0.09228142	0.8	0.2	2.6	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EF098385	8.78843931	0.01234851	0.09303853	0.4	4.8	1	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EF100052	8.77028986	0.01246108	0.09339253	1.2	7.2	3.8	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __g
EU503858	13.6363636	0.00109371	0.04406832	1.6	0	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __Incertae_Sedis
EU504135	11.6666667	0.0029283	0.06579326	5.2	0	0.4	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __Incertae_Sedis
EU454464	10	0.00673795	0.06579326	1	0	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __Incertae_Sedis
AY989982	9.91150442	0.00704278	0.06579326	0	1.6	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __Incertae_Sedis
EU510644	9.91150442	0.00704278	0.06579326	0	50.2	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __Incertae_Sedis
EU510652	9.91150442	0.00704278	0.06579326	2.4	0	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __Incertae_Sedis
EU451858	9.88235294	0.00714619	0.06579326	2.6	0	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __Incertae_Sedis
EF098682	9.88235294	0.00714619	0.06579326	3.8	0	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __Incertae_Sedis
EU512007	9.68634686	0.007882	0.06802406	1	1	9	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __Incertae_Sedis
DQ808013	13.2911392	0.00129977	0.04406832	4.4	0	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __Roseburia
EU504206	10	0.00673795	0.06579326	0	0	1	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __Roseburia
DQ807348	9.91150442	0.00704278	0.06579326	2.4	0	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __Roseburia
EU456198	9.5671028	0.00836623	0.07018886	0.2	2	3.2	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Lachnospiraceae; __Roseburia
EU508322	13.2911392	0.00129977	0.04406832	146	0	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Peptococcaceae; __g
EU507522	10.5456842	0.00512901	0.06579326	0.8	4.4	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Ruminococcaceae; __Anaerotruncus
EU509296	9.57552743	0.00833107	0.07018886	0.8	11.2	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Ruminococcaceae; __Anaerotruncus
AY993804	9.56398467	0.00837929	0.07018886	19	0.4	3.2	Bacteria; __Firmicutes; __Clostridia; __Clostridiales;

							__Ruminococcaceae; __Anaerotruncus
FJ880311	9.14520548	0.01033104	0.08233277	3.4	0.4	0.6	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; Ruminococcaceae; __Anaerotruncus
EU452161	8.61970803	0.01343551	0.09964671	1.6	19	7.6	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; Ruminococcaceae; __Anaerotruncus
EF614895	13.3587786	0.00125655	0.04406832	3.4	0	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; Ruminococcaceae; __g
EU504467	13.3587786	0.00125655	0.04406832	6	0	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; Ruminococcaceae; __g
EU506377	13.3248731	0.00127803	0.04406832	4	0	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; Ruminococcaceae; __g
EF098020	11.6176471	0.00300096	0.06579326	0	13.6	1.4	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; Ruminococcaceae; __g
EU511065	11.4333333	0.00329066	0.06579326	0.2	1.6	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; Ruminococcaceae; __g
EU504517	10.3496296	0.00565726	0.06579326	37.4	0	59.8	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; Ruminococcaceae; __g
EU507046	10.2253165	0.00602006	0.06579326	5	0	0.6	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; Ruminococcaceae; __g
EU510149	9.91150442	0.00704278	0.06579326	0	0	9	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; Ruminococcaceae; __g
AY992826	9.91150442	0.00704278	0.06579326	2.2	0	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; Ruminococcaceae; __g
EU508875	9.91150442	0.00704278	0.06579326	2.4	0	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; Ruminococcaceae; __g
EU510000	9.91150442	0.00704278	0.06579326	1.8	0	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; Ruminococcaceae; __g
DQ815745	9.88235294	0.00714619	0.06579326	0	11	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; Ruminococcaceae; __g
EU505209	9.88235294	0.00714619	0.06579326	0	2	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; Ruminococcaceae; __g
FJ681448	9.88235294	0.00714619	0.06579326	2.6	0	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; Ruminococcaceae; __g
EF097460	9.85996276	0.00722664	0.06579326	6	0	6.4	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; Ruminococcaceae; __g
FJ880035	9.65538462	0.00800497	0.06866917	1.8	0	0.6	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; Ruminococcaceae; __g
AY992012	8.95410526	0.01136687	0.08845037	1.2	14.6	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; Ruminococcaceae; __g
EU508855	8.79117647	0.01233162	0.09303853	9.4	14.6	0.4	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; Ruminococcaceae; __g
EU453498	13.6363636	0.00109371	0.04406832	0	1.4	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; Ruminococcaceae; __Incertae_Sedis
EF098406	13.2911392	0.00129977	0.04406832	0	41.4	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; Ruminococcaceae; __Incetiae_Sedis
EU453982	11.6176471	0.00300096	0.06579326	0	59.8	1.4	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; Ruminococcaceae; __Incetiae_Sedis
AM932668	10.9919321	0.00410329	0.06579326	2.6	0	0.4	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; Ruminococcaceae; __Incetiae_Sedis

EF614814	10.9686441	0.00415135	0.06579326	0.4	4.8	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Ruminococcaceae; __Incertae_Sedis
AY993110	10.0258065	0.00665156	0.06579326	0.8	0	3.6	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Ruminococcaceae; __Incertae_Sedis
EF098043	10	0.00673795	0.06579326	0	1.2	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Ruminococcaceae; __Incertae_Sedis
EU622687	10	0.00673795	0.06579326	1	0	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Ruminococcaceae; __Incertae_Sedis
EU505069	9.88235294	0.00714619	0.06579326	0	2.6	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Ruminococcaceae; __Incertae_Sedis
EU505157	8.81771562	0.01216907	0.09266714	0.6	0	1.4	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Ruminococcaceae; __Incertae_Sedis
EU454374	13.2911392	0.00129977	0.04406832	0	0	7.8	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __Ruminococcaceae; __Oscillibacter
EU506730	11.6898608	0.00289454	0.06579326	1.8	0	23.2	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __uncultured; __g
GQ175414	9.91150442	0.00704278	0.06579326	2.8	0	0	Bacteria; __Firmicutes; __Clostridia; __Clostridiales; __uncultured; __g
EU505577	10.0727273	0.00649733	0.06579326	43	0	62.8	Bacteria; __Firmicutes; __Erysipelotrichi; __Erysipelotrichales; __Erysipelotrichaceae; __Allobaculum
EU510600	9.88235294	0.00714619	0.06579326	0	46.8	0	Bacteria; __Fusobacteria; __Fusobacteria; __SHA-35; __f; __g
AM932639	8.66046512	0.01316449	0.09814779	22.2	133.6	25.8	Bacteria; __Tenericutes; __Mollicutes; __Anaeroplasmatales; __Anaeroplasmataceae; __Anaeroplasma
EU457451	13.2911392	0.00129977	0.04406832	5.4	0	0	Bacteria; __Tenericutes; __Mollicutes; __RF9; __f; __g
EU508311	9.91150442	0.00704278	0.06579326	1.8	0	0	Bacteria; __Tenericutes; __Mollicutes; __RF9; __f; __g
EU454200	9.88235294	0.00714619	0.06579326	178.4	0	0	Bacteria; __Tenericutes; __Mollicutes; __RF9; __f; __g
EU455880	9.14165067	0.01034941	0.08233277	11.2	18	0	Bacteria; __Tenericutes; __Mollicutes; __RF9; __f; __g

*Graphically represented in Supplementary Figure 2e